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GenCore version 4.5

Om nucleic - nucleic search, using sw model

Run on: October 5, 2002, 13:47:39 ; Search time 3997.53 seconds
(without alignments) 3976.994 Million cell updates/sec

Title: US-08-153-397A-1

Perfect score: 3962

Sequence: 1 CGGCGCTGAGACTGGGTTA.....AAAAAAACCGGAATT 3962

Scoring table: IDENTITY_NUC ; Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_lestba:*

2: em_estbum:*

3: em_estin:*

4: em_lestnu:*

5: em_estov:*

6: em_estpl:*

7: em_lestro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_pln:*

16: em_gss_virt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	
1	1720	43.4	2633	11 BC006836	
2	24.2	1010	9 AL539517	BC006836 MUS muscu	
3	815.2	20.6	1019	9 AL528663	AL539517 AL539517
4	814.6	20.6	987	9 AL528664	AL528663 AL528663
5	761.6	19.2	898	9 BM04344	AL528664 AL528664
6	715.8	18.1	770	10 BM04344	BM04344 6033619969
7	715	18.0	948	10 BM257820	BM257820 602969918
8	684	17.3	799	10 BM825634	BM825634 603075658
9	680.4	17.2	715	10 BG912321	BG912321 602806684
10	672.4	17.0	719	10 BE744806	BE744806 60157025
11	672	17.0	744	10 BR345815	BR345815 602017891
12	662.6	16.7	718	10 BI193181	BI193181 60294157
13	660.2	16.7	772	9 AL043251	AL043251 60265985
14	655.6	16.5	912	10 BE304984	BE304984 600947930
15	654.6	16.5	662	10 BF944646	BF944646 60049888
16	653.8	16.5	877	10 BE249888	BE249888 600947930
17	652	16.5	957	10 BE737252	BE737252 601305802

RESULT 1

BC006836

LOCUS BC006836

DEFINITION Mus musculus, similar to discoidin domain receptor family, member

ACCESSION BC006836

VERSION BC006836.1 GI:1471754

KEYWORDS HTC.

SOURCE house mouse.

ORGANISM Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2633)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk Email: cggpbs+e@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BOM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: villaon@bcm.tmc.edu

Villaon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.,

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: <http://image.liln.gov>

Series: IRAK Plate: 16 Row: 0 Column: 14

This clone was selected for full length sequencing because it passed the following selection criteria: hexamer frequency ORF analysis

This clone has the following problem: frame shifted.
Location/Qualifiers

JOURNAL		Unpublished (2001)	
FEATURES	source	COMMENT	Contact: Genoscope
QY		Genoscope - Centre National de Séquençage	BP 191 91055 EVRY cedex - France
QY		Email: sequençage.genoscope.cns.fr, Web : www.genoscope.cns.fr	Location/Qualifiers
Db	1818 ACCTGTGAGGTGACGCCCTAAGATCTGGTCAGTCAGTGTGTC	1877	1. organism="Homo sapiens"
Db	1878 ACAAGGCCACCCCTTGTGAGTACGACAGATGCCACCAAGATG	2313	/db_xref="taxon:9806"
Db	1938 -----CCAGGATGATTCCTGAGGAGTAAGATGTCAGGC	1979	/clone_11b="L1_F1013.FBrl"
QY	2314 TCAAGGACCCACATCATTCGCTGCCGGCGTGTGAGACATG	2433	/dev_stage="pooled tissue" from post conception fetuses (20
Db	1980 TGAAGGACCCAAACATCATTCCGGTGTCTGAGGAGATGTCAGGC	2373	week, 24 week and 26 week)
QY	2434 TGATTAATGACTACATGGAGAAGGGCACCTCTAACCGTCTAGT	2493	/lab_host="DHB08"
Db	2040 TGATCACAGACTACATGGAGATGGCATCTGACCACTCTG	2099	cDNA was primed with a NotI oligo(dT) primer. Five prime
QY	2494 AGGACAAAGCAGCGAGGGGGCCCTGGGACGGCAGCTG	2553	end enriched, double-stranded cDNA was digested with Not I
Db	2100 AGAACAAAGGCCACTCAGGGCTCTGGGACACAGACTG	2159	and cloned into the Not I and Eco RV sites of the
QY	2554 GCTACCAATGCTGCTGAGGCCAGATGCCCTCGGATGGCTAT	2613	PCMVSPORT 6 vector. Library was constructed by Life
Db	2160 GCTACCCATGCTGTACACGGGGGCCAGATGCCCTCGGCTAT	2219	Technologies. Contact : Feng Liang Life Technologies, a
QY	2614 CACTCAACTTGTACAGGGACCTGGCACSGGGACTGGCTAGT	2673	division of Invitrogen, 9800 Medical Center Drive Rockville
Db	2220 CCCTGAACTTGTGATGGGACCTGGCACCGGGACATGGCTGG	2279	Maryland 20850, USA Fax : (1) 301 610 8371 Email :
QY	2674 CCATCAAATGGCAGACTTGTGACGGGACTATGGGGACTAT	2733	http://fulllength.invitrogen.com"
Db	2280 CCATCAAATGGCAGACTTGTGACGGGACTATGGGGATAT	2339	2. URL :
QY	2734 TCGAGGGCGGAGCTGGCCATCCGGGATGGGATGGCAGTCT	2793	3. others
Db	2340 TCCAGGGCGGGGTCTGGCCATCAGTGGATGGCTGGAGTC	2399	
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Db	2400 AGTCACACAGGAGTACGTTGGGCTTGAGTGGACCTGTGG	2459	
QY	2854 TCTGTAGGCCAGCCTTGGCAGCTACCGACGAGGTCATCGA	2913	
Db	2460 TCTGCAGGTGCCAGCCTTGGCACATTACAGTACGGTACG	2519	
QY	2914 AGTCCTCCGAGGAGGGCCCGAGGTTACCTGTGCGGCGCT	2973	
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QY	2974 GCCTATATGAGCTGAGCTGGTGTGAGGACGGGAGCTG	3027	
Db	2580 CCCTGTATGAGCTGCTCCGGTGTGAGCCGGAGCCGAG	2633	
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LOCUS	AL539517	1010 bp mRNA	linear EST 16-FEB-2001
DEFINITION	AL539517 LTI_FL013_FBRn1	Homo sapiens	cdna clone CS0DF033Y015
ACCESSION	AL539517	1010 bp mRNA sequence.	
VERSION	AL539517.1	1	(bases 1 to 1010)
KEYWORDS	EST		L.W.B., Gruber, C., Jesse, J. and Polayes, D.
SOURCE	human.		Full-length cDNA libraries and normalization
ORGANISM	Homo sapiens		
Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1		
AUTHORS	L.W.B., Gruber, C., Jesse, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		

of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies). Note: this is a NIH-MGC library.

of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library.

Query Match	19:2%	Score	761:6	DB 10:	Length	898;	
Best Local Similarity	95.3%	Pred. No.	8.e-128;	Matches	865;	Conservative	
Matches	0;	Mismatches	24;	Indels	9;	Gaps	
QY	2313	GGCAGCTTCCCTGTCTCCAGGATGTTCTGAAAGGGAGAGTCATGTGAGG	2372	Db	2	GGCAGCTTCCCTGTCTCCAGGATGTTCTGAAAGGGAGAGTCATGTGAGG	61
QY	2373	CTCAAGGACCCACATCATCTCGGTGCTGGGGTGTGAGACGACGACCCCCCTGC	2432	Db	62	CTCAAGGACCCACATCATCTCGGTGCTGGGGTGTGAGACGACGACCCCCCTGC	121
QY	2433	ATGATTAATGACTACATGGAGAACGGGAACTCACCAGATGTCCTAGTSCCACCAGCTG	2492	Db	122	ATGATTAATGACTACATGGAGAACGGGAACTCACCAGATGTCCTAGTSCCACCAGCTG	181
QY	2493	GAGGACAGGCAAGGGGGCCCTGGGACGGGAGGAGGGGGCCTGGGAGGGAGGGAGG	2552	Db	182	GAGGACAGGCAAGGGGGCCTGGGACGGGAGGGAGGGAGGGAGG	241
QY	2553	AQCTACCAATGCTGTCATGTTGGCAGGCCAGATGCCCTGGGATGCTGAGGACCC	2612	Db	242	AQCTACCAATGCTGTCATGTTGGCAGGCCAGATGCCCTGGGATGCTGAGGACCC	301
QY	2613	ACACTCAACTTGTACATGGGACCTGSCACCGGAACCTGCTAGTTGGAAATTG	2672	Db	302	ACACTCAACTTGTACATGGGACCTGSCACCGGAACCTGCTAGTTGGAAATTG	361
QY	2673	ACCATCAAAATCCAGACTTGGCATGAGCCGAACCTATGCTGGGACATATTACCGT	2732	Db	362	ACCATCAAAATCCAGACTTGGCATGAGCCGAACCTATGCTGGGACATATTACCGT	421
QY	2733	GTGCAAGGGCCGGCAGTGTCTGGCCATCCGCTGGGAGGCGGAGGAGTCACCTCATGGG	2792	Db	422	GTGCAAGGGCCGGCAGTGTCTGGCCATCCGCTGGGAGGAGTCACCTCATGGG	481
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QY	2853	CTCTGTAAGGCCAGCCCTTGGCAGCTACCCAGGAGCAGGTATCCAGAACCGGGG	2912	Db	542	CTCTGTAAGGCCAGCCCTTGGCAGCTACCCAGGAGCAGGTATCCAGAACCGGGG	601
QY	2913	GAGTCTTCGCGGACCAAGGGCGCGAGGTTACCTGTGTCGGCGGCCCTCTGGCGCGAG	2972	Db	602	GAGTCTTCGCGGACCAAGGGCGCGAGGTTACCTGTGTCGGCGGCCCTCTGGCGCGAG	660
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QY	3146	AGGACACAAATGGCACCCTGACCTTTCCCTCCGGAAAGGCCCATACTTAATAGAG	3202	Db	841	AGGACACAAATGGCACCCTGACCTTTCCCTCCGGAAAGGCCCATACTTAATAGAG	898

LOCUS	BT257820	770	bp	mRNA	Linear	EST	17-JUL-20	
DEFINITION	602969918FL NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109436 5'							
mRNA	sequence.							
REFERENCE	BT257820							
AUTHORS								
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)							
COMMENT	Unpublished (1999)							
KEYWORD	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
1 (bases 1 to 770)								
NIH-MGC http://mgc.nci.nih.gov/ .								
Authors	Robert Strausberg, Ph.D.							
Email:	cgapss-r@mail.nih.gov							
Tissue	procurement: ATCC							
CDNA	Library Preparation: Life Technologies, Inc.							
DNA	Sequencing by: Incyte Genomics, Inc.							
Clone	distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov							
plate: LLAM11265	row: c	column:	05.					
High quality sequence stop: 765.								
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/tissue_type="cervical carcinoma cell line"								
/lab_host="DHIOB"								
/note="Organ: cervix; Vector: PCMV-SPORT6; Site_1: Noti;"								
site_2: Sali; Cloned unidirectionally. Primer: Oligo dT								
Average Insert size 1.4 Kb. Library prepared by Life								
Technologies."								
BASE COUNT	144	a	207	c	262	g	157	
ORIGIN								
Query	Match	18.1%	Score	715.8;	DB	10;	Length	770;
Best local similarity	97.3%	; Pred.	No.	1.7e-119;				
Matches	750;	conservative	0;	Mismatches	17;	Indels	4;	gaps
Db	1	GAAGGTGCTATTCACTAGCGATGGGGTGACTGAAAGATGCCAAGATGCTGCATCTAC	288					
Qy	289	CCACCCCTAGGCCAGGGATCAGGACTATGGGACCTATGGGACAGAGGCCCTGTCATCTAC	348					
Db	61	CCGACCCCTTAGGCCAGGGATCAGGACTATGGGACCTATGGGACAGGCCCTGTCATCTAC	120					
Qy	349	TGCCTGCTCTCTGGGAGAGTCTGAGATCTGAGATGAGAGGATTTGATCCGCCA	408					
Db	121	TGGTGTCTCTTGGTGCAGTGGAGACTGAGATCTGAGATGAGAGGATTTGATCCGCCA	180					
Qy	409	AGTGGCGGTATGCCCTGCGCATGGGACCGGACATCCAGACAGTGAATCTGCTGTT	468					
Db	181	AGTGGCGGTATGCCCTGCGCATGGGACCGGACATCCAGACAGTGAATCTGCTGTT	240					
Qy	469	CCAGCTCTGGTCAGATTCACCTGCCGCCACAGCAGGTGGAGACAGTGAAGGG	588					
Db	241	CCAGCTCTGGTCAGATTCACCTGCCGCCACAGCAGGTGGAGACAGTGAAGGG	300					
Qy	529	ATGGGGCTGGGCCAGGGGGTGGTGGGACGCCAGGAGGAGGAGGAGTGTGGG	588					
Db	301	ATGGGGCTGGGCCAGGGGGTGGTGGGACGCCAGGAGGAGGAGTGTGGG	360					
Qy	589	ATCTACAAAGACTGCACCTGGTGCCTGAGATCTGGGGACGCCAGGAGGAGCAGTGC	648					
Db	361	ATCTACAAAGACTGCACCTGGTGCCTGAGATCTGGGGACGCCAGGAGGAGCAGTGC	420					

QY 649 TGGCAAGGAGTCTCCGGACACTACGGGCTCGTACTCCGGATGGTCCCGCGTGA 708
 DB 421 TGGCAAGGAGTCTCCGGACACTACGGGCTCGTACTCCGGATGGTCCCGCGTGA 480
 QY 709 TGGCGTGAAGGACCTGGGCCCATGGTGGCCACTGGTCGCTTCAGGATGAGGACCTGGAGG 768
 DB 481 TGGCGTGAAGGACCTGGGCCCATGGTGGCCACTGGTCGCTTCAGGATGAGGACCTGGAGG 540
 QY 769 TGGTGTGAAGGACCTGGGCCCATGGTGGCCACTGGTCGCTTCAGGATGAGGACCTGGAGG 828
 DB 541 TGGTGTGAAGGACCTGGGCCCATGGTGGCCACTGGTCGCTTCAGGATGAGGACCTGGAGG 600
 QY 829 CTGACCGGGTCACTG---AGTGTCTGCTGCGGTAGCTGAGCTATGGCTGCTCTGGAGG 885
 DB 601 CTGACCGGGTCACTGAGCAGTCGACTGCGGTAGAGCTATGGCTGCTCTGGAGG 660
 QY 886 ATGGACTCTCTTACACCCCGCTGGCCAGACAGTATTATCTGAGGGCTGT 945
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 QY 946 ACTCACGACTCCACCTATGAGGACATACTGGGGGACTGAGTATG 996
 DB 720 ACCTCAAGGACTCCACCTATGAGGACATACTGGGGGACTGAGTATG 770

RESULT 7
 LOCUS BI:825684 948 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603072688F1 NTH_MGC_119 Homo sapiens cDNA clone IMAGE:5164480 5',
 mRNA sequence.
 ACCESSION BI:825684
 VERSION BI:825684.1 GI:15937234
 KEYWORDS EST, human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 948)
 AUTHORS NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
 VERSION
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL (Unpublished) (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Life Technologies, Inc.
 DNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)
 Email: cgaps-r@mail.nih.gov
 DNA Sequencing by: Incyte Genomics, Inc.
 MCC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at:
<http://Image.llnl.gov>
 Plate: LLM1408 row: h column: 17
 High quality sequence stop: 785.

FEATURES
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 /note="Organ: brain; Vector: PCMV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (Bc0RV site is destroyed upon cloning). Average insert size 1.3 kb. Insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NTH_MGC Library."
 BASE COUNT 178 a 272 c 296 g 202 t
 ORIGIN

Query Match 18.0%; Score 715; DB 10; Length 948;
 Best Local Similarity 93.0%; Pred. No. 2, 3e-119;
 Matches 845; Conservative 0; Mismatches 35; Indels 29; Gaps 8;
 Matches 845; Conservative 0; Mismatches 35; Indels 29; Gaps 8;
 QY 2136 CCTCGATCTCGACTCCCTTCAGGAGAGCTGGCGAGGAGCTGCAC 2195
 DB 1 CTCGATCTCGACTCCCTTCAGGAGAGCTGGCGAGGAGCTGCAC 60
 QY 2196 CGTGTGAGGAGACGCCCTAAGTCGTCAGCTGTTCCCCTAATGCGT 2255
 DB 61 CTCGTTGAGGTGACCCCTCAAGTCGTCAGCTGTTCCCCTAATGCGT 120
 QY 2256 AAGGACACCCCTGTGTAGCTGTCAGAATGCTAGCCACAAATGCC 2315
 DB 121 AAGGACACCCCTGTGTAGCTGTCAGAATGCTAGCCACAAATGCC 222
 QY 2316 AGCTCTCTGTTCTCCASGRATGATTCTGAAGAGGAGATCGCAGGCTC 2375
 DB 179 -----CCAGGATGATTCTGTAAAGAGGGAAGATCATGTCGAGGCTC 222
 QY 2376 AAGGACCCCAACATCATTCGCTGGGGCTGTGTGCGAGGACCCCTCGATG 2435
 DB 223 AAGGACCCCAACATCATTCGCTGGGGCTGTGTGCGAGGACCCCTCGATG 282
 QY 2436 ATTACGACTACATGGAGAAGGGGACCCTCACCGTTCTCAGTGCCACAGCTGGAG 2495
 DB 283 ATTACGACTACATGGAGAAGGGGACCCTCACCGTTCTCAGTGCCACAGCTGGAG 342
 QY 2496 GACAAGGCCGGAGGGGGGCCCTGGAGGGAGGCTGGCGAGGGGCCACCATCAGC 2555
 DB 343 GACAAGGCCGGAGGGGGGCCCTGGAGGGAGGCGAGGCTGGCGACCATCAGC 402
 QY 2556 TACCCATGCTGCTCATGGCATGGGACATGCCATCGCTCTGGCATCGCTG 2615
 DB 403 TACCCATGCTGCTCATGGCATGGGACATGCCATCGCTCTGGCATCGCTG 462
 QY 2616 CTCAACTTGTACATGGACCTGGCCACGGGAAACCTGATGCTAGTGGGACTATTACGGTGC 2675
 DB 463 CTCAACTTGTACATGGACCTGGCCACGGGAAACCTGATGCTAGTGGGACTATTACGGTGC 522
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 DB 523 ATCAAATGGAGACTTGTGATGGCCACGGGAAACCTGATGCTAGTGGGACTATTACGGTGC 582
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 DB 583 CAGGGCGGCCAGCTGGCCATCGCTGATGGCTGGAGTCATCTCAGGGGA 642
 QY 2796 TTCAAGCTGGAGTGGACCTGGGGCTTGGTGA -CCCTGGGGAGGTGTATGATCCTGGGA 2854
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 QY 2855 CTGTAGGGCCAGCCTTGG --CAGTCACCGAGCAGCTGAGACGGGG 2911
 DB 703 CTGTAAGGCCAGCTTGGGAGCTAACCCACGAGGCGAGCTCATCGAGACGGGG 762
 QY 2912 GGAGSTCTTGGGCCAGGGCGCA -GGGTGACCTGTCGGGCC --GGCTGGCTGCC 2967
 DB 763 GGAGTCTTCGGGCCAGGGCGCAAGGTGGCTGGGCCCTGGCTGCC 822
 QY 2968 CGCAGGCTA-TATGAGGTGATCTCGTCTGGAGGGAGTCAGGAGGACCA 3026
 DB 823 CGCAGGCCATTATGGAGCTGCTGGCTGGCTGGAGT -AGCGGGACCA 880
 QY 3027 CCCTTTCC 3035
 DB 881 CCTTTCCC 889

RESULT 8
 LOCUS BG912321 799 bp mRNA linear EST 05-JUN-2001

DEFINITION	60280664FL NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4939239
5'_mRNA sequence.	
ACCESSION	BG312321
VERSTON	BS912321.1 GI:14292797
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 799)
TITLE	NIH-MGC http://mgc.ncbi.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs@email.nih.gov
TISSUE	Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.	
Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution by: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
Plate: LLAM0875 row: 0 column: 16	
High quality sequence stop: 768.	
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	/tissue_type="anaplastic oligodendrogloma with 1p/19q loss"
	/lab_host="BPH10B (T1 phage-resistant)"
	/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT	163 a 238 c 251 g 147 t
ORIGIN	
Query Match	17.3%; score 684; DB 10; Length 799;
Best Local Similarity	95.7%; Pred. No. 9.4c-114; Indels 9; Gaps 5;
Matches	758; Conservative 0; Mismatches 25;
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Db	1 ACTACATGGAGAGGGGACACTAACAGTTCAGTGAGGACAGG 60
QY	CAGCGAGGGGCCCTGGAGGGCAGGCCACCATCACGGTACCCAA 2562
Db	61 CAGCCGAGGGGCCCTGGAGGGCAGGTGGCAGGGCCACCATCAGTACCCAA 120
QY	TGGTGCTCATGGGACCCACATGCTCGGCAAGGGTAACTGCCAACACT 2622
Db	121 TCGAGCTCATGGGACCCACATGCCCTGGCATCGCTTCTGCCAACACT 180
QY	TGGTACATGGGACCTGGCACGGAACTGCTAGTGGGAATTTCACCATCAA 2682
Db	181 TGGTACATGGGACCTGGCACCGGAAGTGTGGAATTTCACCATCAA 240
QY	TGGAGACTTGGCATGGCCACGGAACTGCTAGTGGGAATTTCACCATCAA 2742
Db	241 TCGAGACTTGGCATGGCCACGGAACTTACCGTGGCATCGAGGCC 300
QY	GGGAGTGGTGGCATCGCTGGATGGCTGGAGTGGCATCCATGGGAATTTCACCAA 2802
Db	301 GGAGATGGTGGCATCGCTGGATGGCTGGAGTGGCATCCATGGGAATTTCACCAA 360
QY	CTGGAGTGACGGTGGCCTTGGTGTGACCCGGTGGAGGTGATGCTGTAGG 2862
Db	361 CTGGAGTGACGGTGGCCTTGGTGTGACCCGGTGGAGGTGATGCTGTAGG 420
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	/tissue_type="adenocarcinoma cell line"
	/lab_host="BPH10B (phage-resistant)"
	/note="Organ: ovary; Vector: pOM7; Site_1: XbaI; Site_2: EcoRI; CDNA made by oligo-dT priming. directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGAGCAG (G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and superscript II RT (Life Technologies)."
BASE COUNT	130 a 226 c 212 g 147 t
ORIGIN	
RESULT	9
BE744806	
LOCUS	BE744806
DEFINITION	60151025FL NIH-MGC_9 Homo sapiens cDNA clone IMAGE:3836046
5'	mRNA linear EST 15-SEP-2000
ACCESSION	60151025FL NIH-MGC_9
VERSION	BE744806.1 GI:10158798
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 715)
TITLE	NIH-MGC http://mgc.ncbi.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs@email.nih.gov
TISSUE	Procurement: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov	
Plate: LLM519 row: a column: 07	
High quality sequence stop: 713.	
FEATURES	Location/Qualifiers
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	/db_xref="taxon:9606"
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	/clone_lib="NIH-MGC_9"
	/tissue_type="adenocarcinoma cell line"
	/lab_host="BPH10B (phage-resistant)"
	/note="Organ: ovary; Vector: pOM7; Site_1: XbaI; Site_2: EcoRI; CDNA made by oligo-dT priming. directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGAGCAG (G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and superscript II RT (Life Technologies)."
BASE COUNT	130 a 226 c 212 g 147 t
ORIGIN	
QY	2863 CCGAGCCCTTGGCAGCTACCGACGCCAGGTACCGAGAACCGGGAGTCTCC 2922
Db	421 CCGAGCCCTTGGCAGCTACCGACGCCAGGTACCGAGAACCGGGAGTCTCC 480
QY	2923 GGGACCGGCCGCCAGGTACCGAGAACCGGGAGTCTCC 2981
Db	481 GGGACCGGCCGCCAGGTACCGAGAACCGGGAGTCTCC 540
QY	2982 GAGCTGATGCTGGTGTGGACCGCGAGTCAGGAGGACCCCTTTCACCTG 3041
Db	541 GAGCTGATGCTGGTGTGGACCGCGAGTGTGAGCAGGCCA-CCTTTCCACGTG 599
QY	3042 CATGGTGTCTGGCAGAGTCACTCACACGGTGTGTAATCACAGCTGG 659
Db	600 CATGGTGTCTGGCAGAGTCACTCACACGGTGTGTAATCACAGCTGG 659
QY	3097 CCCCTCCCTAGGGAGGTCCAGGGAGGCCAGTGAACATRAAACAGGACAA 3154
Db	660 CCCTCCCTAGGGAGGTCCAGGGAGGCCAGTGAACATRAAACAGGACAA 719
QY	3155 TGGACCTCTGCCTTCGCCCTCCGACGCCATCACCTTAATAGAGGAGCTGAGCTG 3214
Db	720 TGGACCTCTGCCTTCGCCCTCCGACGCCATCACCTTAATAGAGGCTGAGTGA 779
QY	3215 CAGGTGGCTGG 3226
Db	780 CAGGTGGCTGG 791

Query Match 17.28; Score 680.4; DB 10; length 715;
 Best Local Similarity 99.4%; Pred. No. 4.2e-113;
 Matches 714; Conservative 0; Mismatches 1; Indels 3;
 Gaps 3;

Tissue Procurement: David N. Louis, M.D.
Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)
DNA Sequencing by: Incyte Genomics, Inc.
bioinformatics by: Incyte Genomics, Inc.

QY 2682 ATCGCAGACTTGGCATGACCGGAACTCTATGCTGGGAACTTACCGGTTGCAAGGGC 2741

1 ATTCGCAACTTGGCAGAGCGGGAACTCTATGCTGGGGACTTATTCGGTGTCA - GGC 59
 2742 CGGGCACTGTCGCCATCGCGGATGGGGCTGGAGTCATCTCATGGGAAGTCAG 2801

FEATURES
source
High quality sequence stop: 719.
location/Qualifiers
1. .719

Db	60	CGGGCAGTGTGCCCCATCCCGCTGGGAGGGCCCTGGGAGTCATCTCATGGGAATGTCAGC	119
Qy	2802	ACTGGAGGAGCTGGGCTTGTGGTGTGACCTGTGGAGGGTGTGTGAGTCAGTCAGC	2861

QY	2862	GGCCAGCCTTGGGCCGACGCCAGGAGCAGGTCATCGAGAACGGGGGAGTCTTC	2921
QY	120	ACTCGGAGTGACGTTGGGCTTGGTGACCCGTGGAGGGCTGATGCTGTGAGG	179

Db	180	GGCCAGCCCTTGGGCAAGCTACCCAGGAGCAGGTCTTC	239
QY	2922	CGGACGAAAGGCCGAGGTTACCGTCGGCCCTGTCTGGCGGGAGGCTATA	2981

240 CGGACCAAGGCCGAGGTACCTGTCCTGGCCGCTGCTGCCGGAGGCTATAT 299

QY	3042	CATCGGTCTCTGGCAGAGGTGCACTCAACAGGCTGAAACACATCAGTCGCCCC	3101
Db	360	CATCGGTCTCTGGCAGAGGTGCACTCAACAGGCTGAAACACATCAGTCGCCCC	419

QY	3102	CCCTCAGGGAGTATGCCAGGGAAACCCAGTGACACTTAAACAGAGGACACATGGCAC	3161
	420	CCCTCAGGGAGTCAGGAAACCCAGTGACACTTAAACAGAGGACACATGGCAC	478

479 TCTGGCCCTTACCCCTTCCGAGACCCATCACCTCTAACTAGGCGCTGAGACGAGCAGGRRG 538
 3222 GCTGGGGCCACCCAGGGACTGTGAGCCCTCTCCCTTCTGGACACATCTCATGCG 3281

Db 539 GCGGGCCACCCGGGACCTGGATCCCCCTCTCCCTTCCTGGACACCTCTATGIC 598
 3282 CCTTCCTGTTCTCTCTAGAACGCCCTGTCGCCACCCAGCTGTGTCCTGATGIC 3341

658 ATCTCTCCACCTCTCTAGCCATCCCTGGGAGGGTGGGAGAAATAGGATA 715

RESULT 10
PR345815 BF345815
FOCUS 719 hn mPNA linear PCM 22-Nov-2014

DEFINITION 602017891F1 NCI_CGAP_Brn67_Homo sapiens CDNA clone IMAGE:4153367
5' mRNA sequence
ACCESSION BF345815

BR343815.1 G1:11293410
KEYWORD
EST.
SOURCE
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 19)

NIH-MGC http://mgcc.ncbi.nih.gov/ (MGC)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
COMMENT Contact: Robert Strausberg, Ph.D.

QY	3057	GAGGATCCTACTACCA-CGGTGAATCACACATCCAGCTGCCCTCTCAGGAGTGA	3115	DEFINITION	602947157F1 NIH_MGC_42 Homo sapiens mRNA clone IMAGE:5090223 5'
Db	659	GAGGATCCTACTACCA-CACCGGTTGAATCACATCCAG	717	ACCESSION	BI193181
QY	3116	TC 3117		VERSION	BI193181.1 GI:14648201
Db	718	TC 719		KEYWORDS	EST.
QY	2477	CAGTCGCCACCAAGCTGGAGGACAAGCAGCGAGGGGCCCTGGGACSGGGACTCTG	2476	SOURCE	human.
Db	242	CAGTCGCCACCAAGCTGGAGGACAAGCAGCGAGGGGCCCTGGGACSGGGACTCTG	2476	ORGANISM	Homo sapiens
QY	2537	GCAGGGGCCACCATAGCTTACCCATGCTGCTGATGTGAGCAGTGCCAGTGCC	2595	COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Db	302	GCAGGGGCCACCATAGCTTACCCATGCTGCTGATGTGAGCAGTGCCAGTGCC	2595	REFERENCE	1 (bases 1 to 744) NIH_MGC http://mgc.nci.nih.gov/
QY	2597	CATGGCTATCTGGCACACTCAGTACCCATGCGCTGATGCGACGGGACTGGCGAACATGCGCT	2656	AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
Db	362	CATGGCTATCTGGCACACTCAGTACCCATGCGCTGATGCGACGGGACTGGCGAACATGCGCT	2656	TITLE	Unpublished (1999)
QY	2657	AGTGGGAAATTCACCTCAAAATCAGCTAGACTTGGATGACCCGAACTTATG	2715	JOURNAL	CONTACT: Robert Strausberg, Ph.D.
Db	422	AGTGGGAAATTCACCTCAAAATCAGCTAGACTTGGATGACCCGAACTTATG	2715	COMMENT	Email: cgrabs-r@mail.nih.gov
QY	2717	TGGGACTATTACCGTGTGAGGCAACTTCACACTGGACATGGGACATGGGACATGGGAACTTGCGCT	2775	TISSUE	Procurement: ATCC
Db	482	TGGGACTATTACCGTGTGAGGCAACTTCACACTGGACATGGGACATGGGACATGGGAACTTGCGCT	2775	PROCUREMENT	CDNA Library Preparation: Ling Hong/Rubin Laboratory
QY	2777	GTGGAGGGCTGTGCTGCTGCTGAGCTGGAGTACGTTGGGCTTGGTGTACCT	2836	CDNA	Sequencing by: Incyte Genomics, Inc.
Db	541	GTGCACTCCATGGGAAGTCACCACTGCGAGTGAGTACGTTGGGCTTGGTGTACCT	2836	LIBRARY	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov/plate:LLCM1052 row: b. column: 16
QY	2837	GTGGAGGGCTGTGCTGCTGAGCTGGAGTACGTTGGGCTTGGTGTACCT	2836	ARRANGED	High quality sequence stop: 675.
Db	601	GTGGAGGGCTGTGCTGCTGAGCTGGAGTACGTTGGGCTTGGTGTACCT	2836	LOCATION/QUALIFIERS	Location/Qualifiers
QY	2897	CATCGAGAAG-CGGGAGTCTCCGGACAGGGCGCAGSTGTACGTCCGG	2955	1.	1. .744
Db	660	CATCGAGAAGCGGGAGTCTCCGGACAGGGCGCAGSTGTACGTCCGG	2955	ORGANISM	/organism="Homo sapiens"
QY	2956	CGCCTGCCCTGCC 2967		FEATURES	/db_xref="taxon:9606"
Db	720	CGCCTGCCCTGCC 731		SOURCE	/clone="IMAGE:5090223"
QY	2956	CGCCTGCCCTGCC 2967		COMMENT	/clone_id="NIH_MGC_42"
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QY	2956	CGCCTGCCCTGCC 2967		LOCUS	/lab_host="DH10B (phage-resistant)"
Db	720	CGCCTGCCCTGCC 731		DEFINITION	/note="Organ: pancreas; Vector: pORN7; Site: 1: xhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library.]"
QY	2956	CGCCTGCCCTGCC 2967		ACCESSION	BI193181
Db	720	CGCCTGCCCTGCC 731		VERSION	BI193181.1 GI:14648201
QY	2956	CGCCTGCCCTGCC 2967		KEYWORDS	EST.
Db	720	CGCCTGCCCTGCC 731		ORGANISM	human.
QY	2956	CGCCTGCCCTGCC 2967		COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Db	720	CGCCTGCCCTGCC 731		REFERENCE	1 (bases 1 to 718) NIH_MGC http://mgc.nci.nih.gov/
QY	2237	TTCCGCCCTATGGCGTAAAGGACCCCTTGCTGGTACCTGTCAGATCTAGGGC	2296	TITLE	CDNA Library Preparation: Life Technologies, Inc.
Db	2	TTCCGCCCTATGGCGTAAAGGACCCCTTGCTGGTACCTGTCAGATCTAGGGC	61	JOURNAL	Unpublished (1999)
QY	2297	AGATGCCACCAAGAATGCCACTTCCTCTTCTCAGGATGATGTTCCGAAAGGT	2356	COMMENT	CONTACT: Robert Strausberg, Ph.D.
Db	62	AGATGCCACCAAGAATGCCACTTCCTCTTCTCAGGATGATGTTCCGAAAGGT	2356	PROCUREMENT	Tissue Procurement: James Cleaver, M.D.
QY	2357	GAAGATCATGTCGAGCTGAGGCCAACATCATCGCTGCTGGCGCTGCTG	2416	CDNA	CDNA Library Preparation: Life Technologies, Inc.
Db	122	GAAGATCATGTCGAGCTGAGGCCAACATCATCGCTGCTGGCGCTGCTG	2416	LIBRARY	Sequencing by: Incyte Genomics, Inc.
QY	2417	GGACCAACCCCTCTCATGTTACTGCTACATGGAGAACGGCACCTCACCAGTC	2476	ARRANGED	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov/plate:LLM10696 row: j column: 22
Db	182	GGACCAACCCCTCTCATGTTACTGCTACATGGAGAACGGCACCTCACCAGTC	2476	LOCATION/QUALIFIERS	High quality sequence stop: 717.
QY	242	CAGTCGCCACCAAGCTGGAGGACAAGCAGCGAGGGGCCCTGGGACSGGGACTCTG	301	FEATURES	Location/Qualifiers
Db	720	CGCCTGCCCTGCC 731		SOURCE	1. .718
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Query Match 16.5%; Score 655.6; DB 10; Length 912; Best Local Similarity 95.4%; Pred. No. 1.3e-108; Matches 740; Conservative 0; Mismatches 29; Indels 7; Gaps 6;

BASE COUNT 211 a 244 c 277 g 180 t

ORIGIN

RESULT 14

LOCUS BE304884/c

DEFINITION mRNA sequence.

ACCESSION BE304884

VERSION 1

AUTHORS NIH-MGC

TITLE BE304984.1 GI:9176727

JOURNAL EST.

COMMENT

ORGANISM Homo sapiens

Hom sapiens

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 912)

NIH-MGC <http://mgc.ncbi.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@email.nih.gov

FEATURES

source

1. . 912

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2959015"

/clone_id="NIH-MGC-15"

/tissue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pOTB7; Site-1: XbaI; Site-2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCAGGAG(G)3. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA Synthesis Kit (Stratagene) and Superscript II RT (Life Technologies)"

RESULT 14

LOCUS BE304884

DEFINITION mRNA sequence.

ACCESSION BE304884

VERSION 1

AUTHORS NIH-MGC

TITLE BE304984.1 GI:9176727

JOURNAL EST.

COMMENT

ORGANISM Homo sapiens

Hom sapiens

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 912)

NIH-MGC <http://mgc.ncbi.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@email.nih.gov

FEATURES

source

1. . 912

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2959015"

/clone_id="NIH-MGC-15"

/tissue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pOTB7; Site-1: XbaI; Site-2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCAGGAG(G)3. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA Synthesis Kit (Stratagene) and Superscript II RT (Life Technologies)"

RESULT 15

LOCUS BF944646

DEFINITION mRNA sequence.

ACCESSION PM0-NN1171-181000-001-c05 NN1171

VERSION BF944646.1

AUTHORS

TITLE

RESULT 15

LOCUS BF944646

DEFINITION mRNA sequence.

ACCESSION PM0-NN1171-181000-001-c05 NN1171

VERSION BF944646.1

AUTHORS

TITLE

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2707001
 Fax: +55-11-270701
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM05t2=PM0-NN171-181000-001-c05&t3=2000-10-18&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence/stop: 660.

FEATURES

source

Location/Qualifiers
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 /db_xref="txon:9606"
 /clone lib="NM1171"
 /dev_stage="Adult"
 /note="Organ: nervous-normal; Vector: puc18; Site 1: SMAR,
 Site 2: SMAL; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT
 ORIGIN
 124 a 214 c 191 g 132 t 1 others

Query Match Similarity 16.5%; Score 654.6; DB 10; Length 662;

Best Local Similarity 99.2%; Pred. No. 1.9e-108; Mismatches 5; Indels 0; Gaps 0;

Matches 657; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 2798 CACGACTGGGAGAGCTGGTGGGGCTTGGTGGACCCCTGGGAGGCTGTGCTG 2857
 Db 1 CACGACTGGGAGAGCTGGTGGGGCTTGGTGGACCCCTGGGAGGCTGTGCTG 60
 Qy 2858 TAGGCCGACCCCTGGCAGCTACCCACGGCTGAGCTGGGAGCTGGTGTGCTG 2917
 Db 61 TAGGCCGACCCCTGGCAGCTACCCACGGCTGAGCTGGGAGCTGGTGTGCTG 120
 Qy 2918 CTCGGGACCAAGCCGGCAGCTGACCTGTCCTGGCCGCGCTGGCTGGCCGAGGCT 2977
 Db 121 CTCGGGACCAAGCCGGCAGCTGACCTGTCCTGGCCGCGCTGGCTGGCCGAGGCT 180
 Qy 2978 ATATGAGGTGATCTTCGGCTGGAGCGGGAGCTGAGCAAGGACCCCTGGCA 3037
 Db 181 ATATGAGGTGATCTTCGGCTGGAGCGGGAGCTGAGCAAGGACCCCTGGCA 240
 Qy 3038 GCTGCATCGGTCTGGAGAGATGCACTAACACGGCTGATCACACATCAGCTGC 3097
 Db 241 GCTGCATCGGTCTGGAGAGATGCACTAACACGGCTGATCACACATCAGCTGC 300
 Qy 3098 CCTTCCCTCAGGGAGTGTCAAGGGAGCCATGACATAAACAAAGGAGAACATGG 3157
 Db 301 CCTTCCCTCAGGGAGTGTCAAGGGAGCCATGACATAAACAAAGGAGAACATGG 350
 Qy 3158 CACCTCTGGCTTCCCTCCGAGAGCCATCACCTCTAATAGGGCACTGACTGCAG 3217
 Db 361 CACTCTGGCTTCCCTCCGAGAGCCATCACCTCTAATAGGGCACTGACTGCAG 420
 Qy 3218 GAGGGCTGGGACACCCAGGAGCTGAGCCCTTCCTGACACTCTCAT 3277
 Db 421 GAGGGCTGGGACACCCAGGAGCTGAGCCCTTCCTGACACTCTCAT 480
 Qy 3278 GRCGCCCTCTCTCTCTCTCTAGAGCCCTGGCCACCCAGCTGGCTCTGGA 3337
 Db 481 GRCGCCCTCTCTCTCTCTAGAGCCCTGGCCACCCAGCTGGCTCTGGA 540

Search completed: October 5, 2002, 16:12:29
 Job time: 8690 sec

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 Db 541 TGGGATCCTCCACCCCTCTAGCCATCCCTGGGAGGGTGGGAGRAATAGGA 600
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 Db 601 TAGACATGGGACATGGCCATGGGAGCCACCTGGGACACACTGATTCCTG 660
 Qy 3458 AG 3459
 Db 661 AG 662